CCACGCGTCCGGTCAGCTCTGGTTCGGAGAAGCAGCGGCTGGCGTGGGCCATCCGGGGAATGGGC
GCCCTCGTGACCTAGTGTTGCGGGGCAAAAAGGGTCTTGCCGGCCTCGCTCGTGCAGGGGCGTAT
CTGGGCGCCTGAGCGCGGCGTGGGAGCCTTGGGAGCCGCCGCAGCAGGGGGCACACCCGGAACCG
GCCTGAGCGCCCGGGACCATGAACGGGGAGGCCATCTGCAGCGCCCTGCCCACCATTCCCTACCA
CAAACTCGCCGACCTGCGCTACCTGAGCCGCGGCGCCTCTGGCACTGTGTCGTCCGCCCGCCACG
CAGACTGGCGCGTCCAGGTGGCCGTGAAGCACCTGCACATCCACACTCCGCTGCTCGACAGTGAA
AGAAAGGATGTCTTAAGAGAAGCTGAAATTTTACACAAAGCTAGATTTAGTTACATTCTTCCAAT
TTTGGGAATTTGCAATGAGCCTGAATTTTTGGGAATAGTTACTGAATACATGCCAAATGGATCAT
TAAATGAACTCCTACATAGGAAAACTGAATATCCTGATGTTGCTTGGCCATTGAGATTTCCCATC
CTGCATGAAATTGCCCTTGGTGTAAATTACCTGCACAATATGACTCCTCCTTTACTTCATCATGA
CTTGAAGACTCAGAATATCTTATTGGACAATGAATTTCATGTTAAGATTGCAGATTTTGGTTTAT
CAAAGTGGCGCATGATGTCCCTCTCACAGTCACGAAGTAGCAAATCTGCACCAGAAGGAGGGACA
ATTATCTATATGCCACCTGAAAACTATGAACCTGGACAAAAATCAAGGGCCAGTATCAAGCACGA
TATATATAGCTATGCAGTTATCACATGGGAAGTGTTATCCAGAAAACAGCCTTTTGAAGATGTCA
CCAATCCTTTGCAGATAATGTATAGTGTGTCACAAGGACATCGACCTGTTATTAATGAAGAAAGT
TTGCCATATGATATACCTCACCGAGCACGTATGATCTCTCTAATAGAAAGTGGATGGGCACAAAA
TCCAGATGAAAGACCATCTTTCTTAAAATGTTTAATAGAACTTGAACCAGTTTTGAGAACATTTG
AAGAGATAACTTTTCTTGAAGCTGTTATTCAGCTAAAGAAAACAAAGTTACAGAGTGTTTCAAGT
GCCATTCACCTATGTGACAAGAAGAAAATGGAATTATCTCTGAACATACCTGTAAATCATGGTCC
ACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGGTTCTCCTGAAACTTCAAGGT
CCCTGCCAGCTCCTCAAGACAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAG
CTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATT
CTGTGATCACAAGACCATTCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACT
CAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAAC
CAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAA
AGAGGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACA
CTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAAACAA
ATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCA
AAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCATAAAAGGATATTTATAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:1)

FIG. 1

Met	Asn	Gly	Glu	Ala	Ile	Cys	Ser	Ala	Leu	Pro	Thr	Ile	Pro	Tyr	His	Lys	Leu	Ala	Asp	20
Leu	Arg	Tyr	Leu	Ser	Arg	Gly	Ala	Ser	Gly	Thr	Val	Ser	Ser	Ala	Arg	His	Ala	Asp	Trp	40
Arg	Val	Gln	Val	Ala	Val	Lys	His	Leu	His	Ile	His	Thr	Pro	Leu	Leu	Asp	Ser	Glu	Arg	60
Lys	Asp	Val	Leu	Arg	Glu	Ala	Glu	Ile	Leu	His	Lys	Ala	Arg	Phe	Ser	Tyr	Ile	Leu	Pro	80
Ile	Leu	Gly	Ile	Cys	Asn	Glu	Pro	Glu	Phe	Leu	Gly	Ile	Val	Thr	Glu	Tyr	Met	Pro	Asn	100
Gly	Ser	Leu	Asn	Glu	Leu	Leu	His	Arg	Lys	Thr	Glu	Tyr	Pro	Asp	Val	Ala	Trp	Pro	Leu	120
Arg	Phe	Arg	Ile	Leu	His	Glu	Ile	Ala	Leu	Gly	Val	Asn	Tyr	Leu	His	Asn	Met	Thr	Pro	140
Pro	Leu	Leu	His	His	Asp	Leu	Lys	Thr	Gln	Asn	Ile	Leu	Leu	Asp	Asn	Glu	Phe	His	Val	160
Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Trp	Arg	Met	Met	Ser	Leu	Ser	Gln	Ser	Arg	Ser	180
Ser	Lys	Ser	Ala	Pro	Glu	Gly	Gly	Thr	Ile	Ile	Tyr	Met	Pro	Pro	Glu	Asn	Tyr	Glu	Pro	200
Gly	Gln	Lys	Ser	Arg	Ala	Ser	Ile	Lys	His	Asp	Ile	Tyr	Ser	Tyr	Ala	Val	Ile	Thr	Trp	220
Glu	Val	Leu	Ser	Arg	Lys	Gln	Pro	Phe	Glu	Asp	Val	Thr	Asn	Pro	Leu	Gln	Ile	Met	Tyr	240
Ser	Val	Ser	Gln	Gly	His	Arg	Pro	Val	Ile	Asn	Glu	Glu	Ser	Leu	Pro	Tyr	Asp	Ile	Pro	260
His	Arg	Ala	Arg	Met	Ile	Ser	Leu	Ile	Glu	Ser	Gly	Trp	Ala	Gln	Asn	Pro	Asp	Glu	Arg	280
Pro	Ser	Phe	Leu	Lys	Cys	Leu	Ile	Glu	Leu	Glu	Pro	Val	Leu	Arg	Thr	Phe	Glu	Glu	Ile	300
Thr	Phe	Leu	Glu	Ala	Val	Ile	Gln	Leu	Lys	Lys	Thr	Lys	Leu	Gln	Ser	Val	Ser	Ser	Ala	320
Ile	His	Leu	Cys	Asp	Lys	Lys	Lys	Met	Glu	Leu	Ser	Leu	Asn	Ile	Pro	Val	Asn	His	Gly	340
Pro	Gln	Glu	Glu	Ser	Cys	Gly	Ser	Ser	Gln	Leu	His	Glu	Asn	Ser	Gly	Ser	Pro	Glu	Thr	360
Ser	Arg	Ser	Leu	Pro	Ala	Pro	Gln	Asp	Asn	Asp	Phe	Leu	Ser	Arg	Lys	Ala	Gln	Asp	Cys	380
Tyr	Phe	Met	Lys	Leu	His	His	Cys	Pro	Gly	Asn	His	Ser	Trp	Asp	Ser	Thr	Ile	Ser	Gly	400
Ser	Gln	Arg	Ala	Ala	Phe	Cys	Asp	His	Lys	Thr	Ile	Pro	Cys	Ser	Ser	Ala	Ile	Ile	Asn	420
Pro	Leu	Ser	Thr	Ala	Gly	Asn	Ser	Glu	Arg	Leu	Gln	Pro	Gly	Ile	Ala	Gln	Gln	Trp	Ile	440
Gln	Ser	Lys	Arg	Glu	Asp	Ile	Val	Asn	Gln	Met	Thr	Glu	Ala	Cys	Leu	Asn	Gln	Ser	Leu	460
Asp	Ala	Leu	Leu	Ser	Arg	Asp	Leu	Ile	Met	Lys	Glu	Asp	Tyr	Glu	Leu	Val	Ser	Thr	Lys	480
Pro	Thr	Arg	Thr	Ser	Lys	Val	Arg	Gln	Leu	Leu	Asp	Thr	Thr	Asp	Ile	Gln	Gly	Glu	Glu	500
Phe	Ala	Lys	Val	Ile	Val	Gln	Lys	Leu	Lys	Asp	Asn	Lys	Gln	Met	Gly	Leu	Gln	Pro	Tyr	520
Pro	Glu	Ile	Leu	Val	Val	Ser	Arg	Ser	Pro	Ser	Leu	Asn	Leu	Leu	Gln	Asn	Lys	Ser	Met	540

(SEQ ID NO:2)

FIG. 2

TTTTTATGGG AATCGCAGCT TGGAAGAGAC AGARCAATTC CAGAAWTAAA TTGRAATTGA
AGATTTAACC AATGTTGTTT TAAAATATTC TAACTTCAAA GAATGATGCC AGAACTTWAA
AAGGGRCTGC GCAGAGTAGC AGGGGCCCTG GAGGGCGCGG CCTGAATCCT GATTGCCCTT
CTGCTGAGAG GACACACGCA GCTGAAGATG AATTTGGGAA AAGTAGCCGC TTGCTACTTT
AACTATGGAA GAGCAGGGCC ACAGTGAGAT GGAAATAATC CCATCAGAGT CTCACCCCCA
CATTCAATTA CTGAAAAGCA ATCGGGAACT TCTGGTCACT CACATCCGCA ATACTCAGTG
TCTGGTGGAC AACTTGCTGA AGAATGACTA CTTCTCGGCC GAAGATGCGG AGATTGTGTG
TGCCTGCCCC ACCCAGCCTG ACAAGGTCCG CAAAATTCTG GACCTGGTAC AGAGCAAGGG
CGAGGAGGTG TCCGAGTTCT TCCTCTACTT GCTCCAGCAA CTCGCAGATG CCTACGTGGA
CCTCAGGCCT TGGCTGCTGG AGATCGGCTT CTCCCCTTCC CTGCTCACTC AGAGCAAAGT
CGTGGTCAAC ACTGACCCAG TGAGCAGGTA TACCCAGCAG CTGCGACACC ATCTGGGCCG
TGACTCCAAG TTCGTGCTGT GCTATGCCCA GAAGGAGGAG CTGCTGCTGG AGGAGATCTA
CATGGACACC ATCATGGAGC TGGTTGGCTT CAGCAATGAG AGCCTGGGCA GCCTGAACAG
CCTGGCCTGC CTCCTGGACC ACACCACCGG CATCCTCAAT GAGCAGGGTG AGACCATCTT
CATCCTGGGT GATGCTGGGG TGGGCAAGTC CATGCTGCTA CAGCGGCTGC AGAGCCTCTG
GGCCACGGGC CGGCTAGACG CAGGGGTCAA ATTCTTCTTC CACTTTCGCT GCCGCATGTT
CAGCTGCTTC AAGGAAAGTG ACAGGCTGTG TCTGCAGGAC CTGCTCTTCA AGCACTACTG
CTACCCAGAG CGGGACCCCG AGGAGGTGTT TGCCTTCCTG CTGCGCTTCC CCCACGTGGC
CCTCTTCACC TTCGATGGCC TGGACGAGCT GCACTCGGAC TTGGACCTGA GCCGCGTGCC
TGACAGCTCC TGCCCCTGGG AGCCTGCCCA CCCCCTGGTC TTGCTGGCCA ACCTGCTCAG
TGGGAAGCTG CTCAAGGGGG CTAGCAAGCT GCTCACAGCC CGCACAGGCA TCGAGGTCCC
GCGCCAGTTC CTGCGGAAGA AGGTGCTTCT CCGGGGCTTC TCCCCCAGCC ACCTGCGCGC
CTATGCCAGG AGGATGTTCC CCGAGCGGGC CCTGCAGGAC CGCCTGCTGA GCCAGCTGGA
GGCCAACCCC AACCTCTGCA GCCTGTGCTC TGTGCCCCTC TTCTGCTGGA TCATCTTCCG
GTGCTTCCAG CACTTCCGTG CTGCCTTTGA AGGCTCACCA CAGCTGCCCG ACTGCACGAT
GACCCTGACA GATGTCTTCC TCCTGGTCAC TGAGGTCCAT CTGAACAGGA TGCAGCCCAG
CAGCCTGGTG CAGCGGAACA CACGCAGCCC AGTGGAGACC CTCCACGCCG GCCGGGACAC
TCTGTGCTCG CTGGGGCAGG TGGCCCACCG GGGCATGGAG AAGAGCCTCT TTGTCTTCAC
CCAGGAGGAG GTGCAGGCCT CCGGGCTGCA GGAGAGAGAC ATGCAGCTGG GCTTCCTGCG
GGCTTTGCCG GAGCTGGGCC CCGGGGGTGA CCAGCAGTCC TATGAGTTTT TCCACCTCAC
CCTCCAGGCC TTCTTTACAG CCTTCTTCCT CGTGCTGGAC GACAGGGTGG GCACTCAGGA
GCTGCTCAGG TTCTTCCAGG AGTGGATGCC CCCTGCGGGG GCAGCGACCA CGTCCTGCTA

FIG. 3A

TCCTCCCTTC CTCCCGTTCC AGTGCCTGCA GGGCAGTGGT CCGGCGCGGG AAGACCTCTT
CAAGAACAAG GATCACTTCC AGTTCACCAA CCTCTTCCTG TGCGGGCTGT TGTCCAAAGC
CAAACAGAAA CTCCTGCGGC ATCTGGTGCC CGCGGCAGCC CTGAGGAGAA AGCGCAAGGC
CCTGTGGGCA CACCTGTTTT CCAGCCTGCG GGGCTACCTG AAGAGCCTGC CCCGCGTTCA
GGTCGAAAGC TTCAACCAGG TGCAGGCCAT GCCCACGTTC ATCTGGATGC TGCGCTGCAT
CTACGAGACA CAGAGCCAGA AGGTGGGGCA GCTGGCGGCC AGGGGCATCT GCGCCAACTA
CCTCAAGCTG ACCTACTGCA ACGCCTGCTC GGCCGACTGC AGCGCCCTCT CCTTCGTCCT
GCATCACTTC CCCAAGCGGC TGGCCCTAGA CCTAGACAAC AACAATCTCA ACGACTACGG
CGTGCGGGAG CTGCAGCCCT GCTTCAGCCG CCTCACTGTT CTCAGACTCA GCGTAAACCA
GATCACTGAC GGTGGGGTAA AGGTGCTAAG CGAAGAGCTG ACCAAATACA AAATTGTGAC
CTATTTGGGT TTATACAACA ACCAGATCAC CGATGTCGGA GCCAGGTACG TCACCAAAAT
CCTGGATGAA TGCAAAGGCC TCACGCATCT TAAACTGGGA AAAAACAAAA TAACAAGTGA
AGGAGGGAAG TATCTCGCCC TGGCTGTGAA GAACAGCAAA TCAATCTCTG AGGTTGGGAT
GTGGGGCAAT CAAGTTGGGG ATGAAGGAGC AAAAGCCTTC GCAGAGGCTC TGCGGAACCA
CCCCAGCTTG ACCACCCTGA GTCTTGCGTC CAACGGCATC TCCACAGAAG GAGGAAAGAG
CCTTGCGAGG GCCCTGCAGC AGAACACGTC TCTAGAAATA CTGTGGCTGA CCCAAAATGA
ACTCAACGAT GAAGTGGCAG AGAGTTTGGC AGAAATGTTG AAAGTCAACC AGACGTTAAA
GCATTTATGG CTTATCCAGA ATCAGATCAC AGCTAAGGGG ACTGCCCAGC TGGCAGATGC
GTTACAGAGC AACACTGGCA TAACAGAGAT TTGCCTAAAT GGAAACCTGA TAAAACCAGA
GGAGGCCAAA GTCTATGAAG ATGAGAAGCG GATTATCTGT TTCTGAGAGG ATGCTTTCCT
GTTCATGGGG TTTTTGCCCT GGAGCCTCAG CAGCAAATGC CACTCTGGGC AGTCTTTTGT
GTCAGTGTCT TAAAGGGGCC TGCGCAGGCG GGACTATCAG GAGTCCACTG CCTYCATGAT
GCAAGCCAGC TTCCTGTGCA GAAGGTCTGG TCGGCAAACT CCCTAAGTAC CCGCTACAAT
TCTGCAGAAA AAGAATGTGT CTTGCGAGCT GTTGTAGTTA CAGTAAATAC ACTGTGAAGA
GAAAAAAAAA ACGGACGCGT GG (SEQ ID NO:7)

FIG. 3B

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCACPTQP
DKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRPWLLEIGFSPSLLTQSKVVVNTDPVSRYT
QQLRHHLGRDSKFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLNSLACLLDHTTGILNEQG
ETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFFHFRCRMFSCFKESDRLCLQDLLFKHYCY
PERDPEEVFAFLLRFPHVALFTFDGLDELHSDLDLSRVPDSSCPWEPAHPLVLLANLLSGKLLKG
ASKLLTARTGIEVPRQFLRKKVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSV
PLFCWIIFRCFQHFRAAFEGSPQLPDCTMTLTDVFLLVTEVHLNRMQPSSLVQRNTRSPVETLHA
GRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALPELGPGGDQQSYEFFHLTL
QAFFTAFFLVLDDRVGTQELLRFFQEWMPPAGAATTSCYPPFLPFQCLQGSGPAREDLFKNKDHF
QFTNLFLCGLLSKAKQKLLRHLVPAAALRRKRKALWAHLFSSLRGYLKSLPRVQVESFNQVQAMP
TFIWMLRCIYETQSQKVGQLAARGICANYLKLTYCNACSADCSALSFVLHHFPKRLALDLDNNNL
NDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSEELTKYKIVTYLGLYNNQITDVGARYVTKIL
DECKGLTHLKLGKNKITSEGGKYLALAVKNSKSISEVGMWGNQVGDEGAKAFAEALRNHPSLTTL
SLASNGISTEGGKSLARALQQNTSLEILWLTQNELNDEVAESLAEMLKVNQTLKHLWLIQNQITA
KGTAQLADALQSNTGITEICLNGNLIKPEEAKVYEDEKRIICF **(SEQ ID NO:8)**

FIG. 4

CACGCGTCCGACTTGCTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTGTGT
GTGCCTGCCCCACCCAGCCTGACAAGGTCCGCAAAATTCTGGACCTGGTACAGAGCAAG
GGCGAGGAGGTGTCCGAGTTCTTCCTCTACTTGCTCCAGCAACTCGCAGATGCCTACGT
GGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCCAGTGAGCAGGTATACCCAGCAGCTGCGACACCATCTG
GGCCGTGACTCCAAGTTCGTGCTGTGCTATGCCCAGAAGGAGGAGCTGCTGCTGGAGGA
GATCTACATGGACACCATCATGGAGCTGGTTGGCTTCAGCAATGAGAGCCTGGGCAGCC
TGAACAGCCTGGCCTGCCTCCTGGACCACACCACCGGCATCCTCAATGAGCAGGGTGAG
ACCATCTTCATCCTGGGTGATGCTGGGGTGGGCAAGTCCATGCTGCTACAGCGGCTGCA
GAGCCTCTGGGCCACGGGCCGGCTAGACGCAGGGGTCAAATTCTTCTTCCACTTTCGCT
GCCGCATGTTCAGCTGCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTC
AAGCACTACTGCTACCCAGAGCGGGACCCCGAGGAGGTGTTTGCCTTCCTGCTGCGCTT
CCCCCACGTGGCCCTCTTCACCTTCGATGGCCTGGACGAGCTGCACTCGGACTTGGACC
TGAGCCGCGTGCCTGACAGCTCCTGCCCCTGGGAGCCTGCCCACCCCCTGGTCTTGCTG
GCCAACCTGCTCAGTGGGAAGCTGCTCAAGGGGCTAGCAAGCTGCTCACAGCCCGCAC
AGGCATCGAGGTCCCGCGCCAGTTCCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCC
CCAGCCACCTGCGCGCCTATGCCAGGAGGATGTTCCCCGAGCGGGCCCTGCAGGACCGC
CTGCTGAGCCAGCTGGAGGCCAACCCCAACCTCTGCAGCCTGTGCTCTGTGCCCCTCTT
CTGCTGGATCATCTTCCGGTGCTTCCAGCACTTCCGTGCTGCCTTTGAAGGCTCACCAC
AGCTGCCCGACTGCACGATGACCCTGACAGATGTCTTCCTCCTGGTCACTGAGGTCCAT
CTGAACAGGATGCAGCCCAGCAGCCTGGTGCAGCGGAACACACGCAGCCCAGTGGAGAC
CCTCCACGCCGGCCGGGACACTCTGTGCTCGCTGGGGCAGGTGGCCCACCGGGGCATGG
AGAAGAGCCTCTTTGTCTTCACCCAGGAGGAGGTGCAGGCCTCCGGGCTGCAGGAGAGA
GACATGCAGCTGGGCTTCCTGCGGGCTTTGCCGGAGCTGGGCCCCGGGGGTGACCAGCA
GTCCTATGAGTTTTTCCACCTCAGCCTCCTCACCTGTAAAACTGGGATCCCAGTATAGA
CTTTGGAAATCAGTAGACACCATATGCTTCAAAAAACAGGGGCTATTAAAATGACATCA
GGAGCCAGAAAGTCTCATGGCTGTGCTTTCTCTTGAAGTTTATACAACAACCAGATCAC
CGATGTCGGAGCCAGACTGGGAAAAAACAAAATAACAAGTGAAGGAGGGAAGTATCTCG
CCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTTGGGATGTGGGGCAATCAAGTT
GGGGATGAAGGAGCAAAAGCCTTCGCAGAGGCTCTGCGGAACCACCCCAGCTTGACCAC
CCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCTTGCGAGGGCCC
TGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACTCAACGATGAA
GTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCATTTATGGCT
TATCCAGAATCAGATCACAGTCTTTTGTGTCAGTGTCTTAAAGGGGCCTGCGCAGGCGG
GACTATCAGGAGTCCACTGCCTCCATGATGCAAGCCAGCTTCCTGTGCAGAAGGTCTGG
TCGGCAAACTCCCTAAGTACCCGCTACAATTCTGCAGAAAAAGAATGTGTCTTGCGAGC
TGTTGTAGTTACAGTAAATACACTGTGAAGAGACTTTATTGCCTATTATAATTATTTTT
ATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACAGAGGAGGCCAGCCTCACCTCATTC
CAACACCTGCCATAGGGACCAACGGGAGCGAGTTGGTCACCGCTCTTTTCATTGAAGAG
TTGAGGATGTGGCACAAAGTTGGTGCCAAGCTTCTTGAATAAAACGTGTTTGATGGATT
AGTATTATACCTGAAATATTTTCTTCCTTCTCAGCACTTTCCCATGTATTGATACTGGT
CCCACTTCACAGCTGGAGACACCGGAGTATGTGCAGTGTGGGATTTGACTCCTCCAAGG
TTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGGGCTTTTAATTTTAATCCTG
GAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAGCTCTTAGCTGGTCTAAGA
ATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTCCTCTGCTAGGCTACCCT
CCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTGGGAAGAAGTGATTCTG
TCCCTCCAAAGAAATAGGGCATGGCTTGCCCCTGTGGCCCTGGCATCCAAATGGCTGCT
TTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCCTGCCTCCCAAGCAGCTGAAG
GGTGACTAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAACTGGGCCAGCAGAGCAT
GTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAGGGTGGGGGTGAT
ACTACTAGATCACTTGTCCTCTTGCCAGCTCATTTGTTAATAAAATACTGAAAACACAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA (SEQ ID NO:25)

FIG. 5

HASDLLKNDYFSAEDAEIVCACPTQPDKVRKILDLVQSKGEEVSEFFLYLL
QQLADAYVDLRPWLLEIGFSPSLLTQSKVVVNTDPVSRYTQQLRHHLGRDS
KFVLCYAQKEELLLEEIYMDTIMELVGFSNESLGSLNSLACLLDHTTGILN
EQGETIFILGDAGVGKSMLLQRLQSLWATGRLDAGVKFFFHFRCRMFSCFK
ESDRLCLQDLLFKHYCYPERDPEEVFAFLLRFPHVALFTFDGLDELHSDLD
LSRVPDSSCPWEPAHPLVLLANLLSGKLLKGASKLLTARTGIEVPRQFLRK
KVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSVPLFCWI
IFRCFQHFRAAFEGSPQLPDCTMTLTDVFLLVTEVHLNRMQPSSLVQRNTR
SPVETLHAGRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFL
RALPELGPGGDQQSYEFFHLSLLTCKTGIPV **(SEQ ID NO:26)**

FIG. 6

SEQ. ID NO. 31/32/33/34

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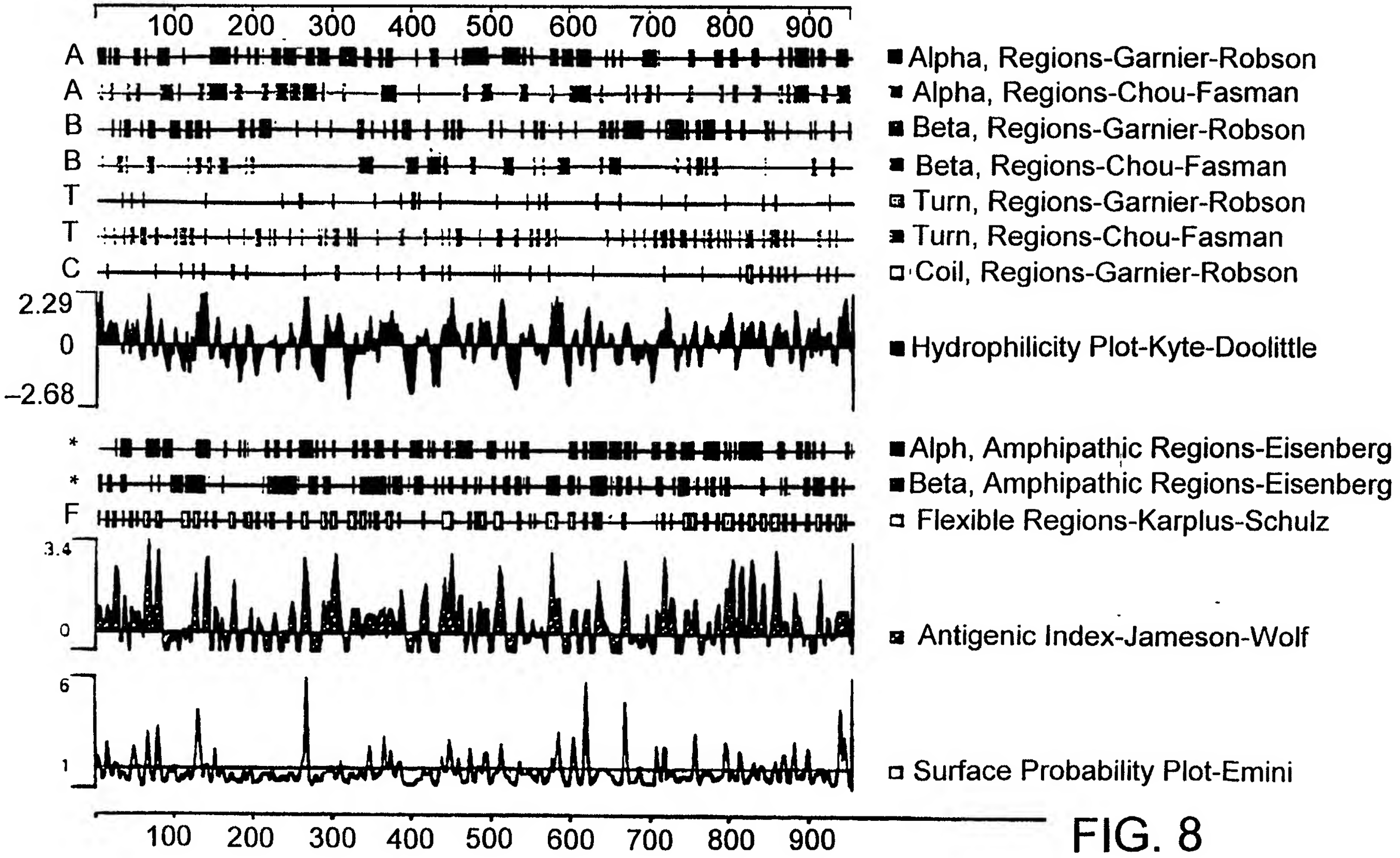
                10        20        30        40
1   E S H P H I - - Q L L K S N R E L L V T H I R N T Q C L - - - V D N L L K N D Y   CARD4-CARD
1   L - Q P G I A Q Q W I Q S K R E D I V N Q M T E A - C L N Q S L D A L L S R D L   CARD3-CARD
1   A Q E R - - P S E T I D R E R K R L V E T L Q A D S G L L - - L D A L L A R G V   ARC-CARD
1   M A S D D L S - - L I R K N R M A L F Q Q L T - - - C V L P I L D N L L K A N V   cIAP1-CARD
1   K E S N D L L - - L I R K N R M A L F Q H L T - - - C V I P I L D S L L T A G I   cIAP2-CARD

                50        60        70        80
36  F S A E D A E I V C A C P T Q P D K V R K I L D L V Q S K G E E V S E F F L Y L   CARD4-CARD
39  I M K E D Y E L V S T K P T R T S K V R Q L L D T T D I Q G E E F A K V I V Q K   CARD3-CARD
37  L T G P E Y E A L D A L P D A E R R V R R L L L L V Q G K G E A A C Q E L L R C   ARC-CARD
36  I N K Q E H D I I K Q K T Q I P L Q A R E L I D T I W V K G N A A A N I F K N C   cIAP1-CARD
36  I N E Q E H D V I K Q K T Q T S L Q A R E L I D T I L V K G N I A A T V F R N S   cIAP2-CARD

                90        100
76  L Q Q L A D A Y V D L R P W - - L L E I G F S P S L L   CARD4-CARD
79  L K D N K Q - - M G L Q P Y P E I L V V S R S P S L     CARD3-CARD
77  A Q R T A G A P D P A W D W Q H V G                     ARC-CARD
76  L K E I D S T L - - - - - - Y K N L - - - - - - - - F V   cIAP1-CARD
76  L Q E A E A V L - - - - - - Y E H L - - - - - - - - F V   cIAP2-CARD
```

FIG. 7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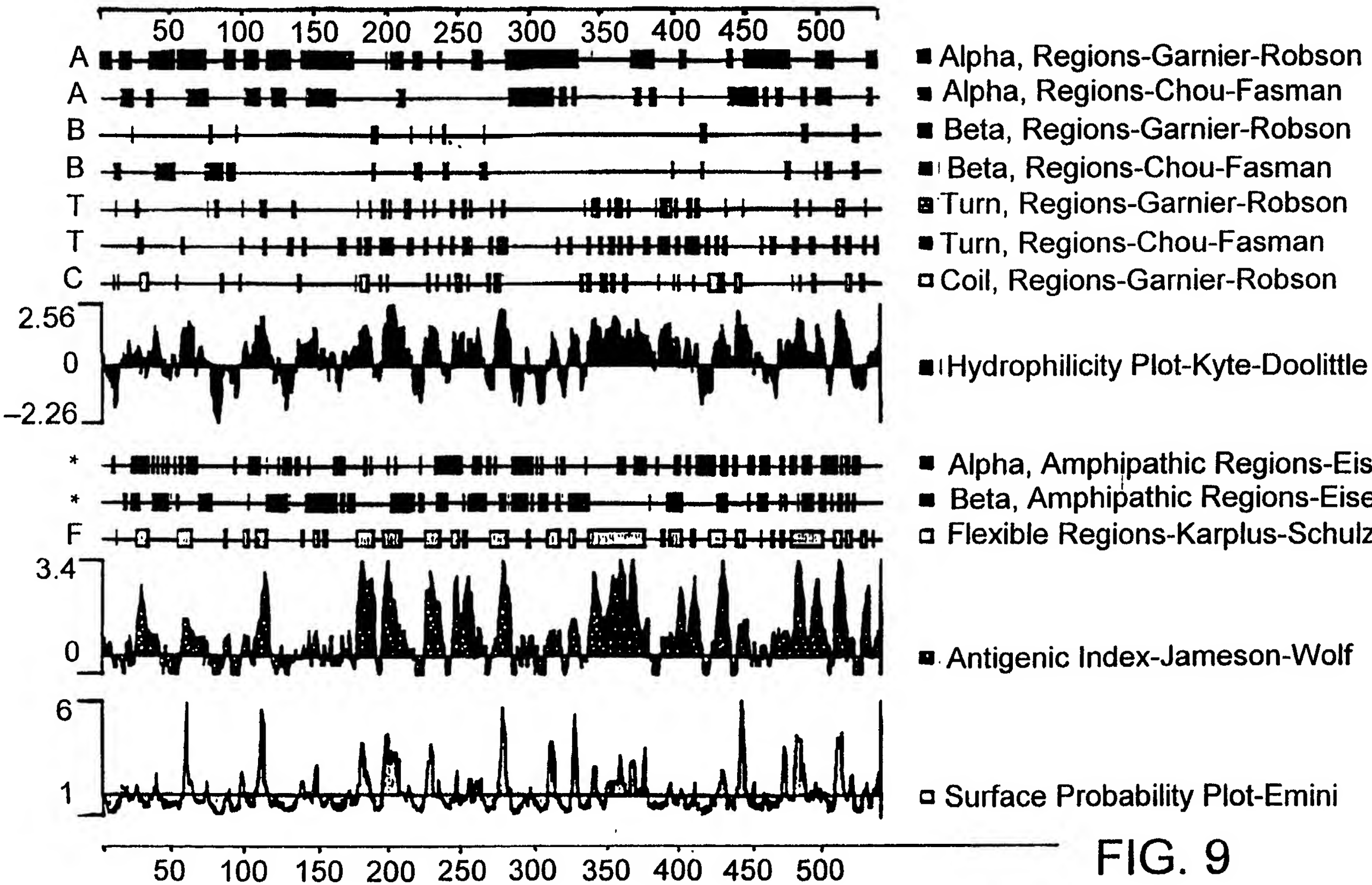
A
A
B
B
T
T
C
2.29
0
–2.68
*
*
F
3.4
0
6
1
100 200 300 400 500 600 700 800 900
Alpha, Regions-Garnier-Robson
Alpha, Regions-Chou-Fasman
Beta, Regions-Garnier-Robson
Beta, Regions-Chou-Fasman
Turn, Regions-Garnier-Robson
Turn, Regions-Chou-Fasman
Coil, Regions-Garnier-Robson
Hydrophilicity Plot-Kyte-Doolittle
Alph, Amphipathic Regions-Eisenberg
Beta, Amphipathic Regions-Eisenberg
Flexible Regions-Karplus-Schulz
Antigenic Index-Jameson-Wolf
Surface Probability Plot-Emini

FIG. 8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A
A
B
B
T
T
C
2.56
0
–2.26
*
*
F
3.4
0
6
1
50 100 150 200 250 300 350 400 450 500
Alpha, Regions-Garnier-Robson
Alpha, Regions-Chou-Fasman
Beta, Regions-Garnier-Robson
Beta, Regions-Chou-Fasman
Turn, Regions-Garnier-Robson
Turn, Regions-Chou-Fasman
Coil, Regions-Garnier-Robson
Hydrophilicity Plot-Kyte-Doolittle
Alpha, Amphipathic Regions-Eisenberg
Beta, Amphipathic Regions-Eisenberg
Flexible Regions-Karplus-Schulz
Antigenic Index-Jameson-Wolf
Surface Probability Plot-Emini

FIG. 9